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NiceZyme View of ENZYME: EC 3.2.1.23

Official Name

Beta-galactosidase.

Alternative Name(s)

Exo-(1->4)-beta-D-galactanase.

Lactase.

Reaction catalysed

Hydrolysis of terminal non-reducing beta-D-galactose residues in beta-D-galactosides

Comment(s)

Some enzymes in this group hydrolyze alpha-L-arabinosides; some animal enzymes also hydrolyze beta-D-fucosides and beta-D-glucosides (cf. EC 3.2.1.108).

Human Genetic Disease(s)

Gangliosidosis,
generalized GM1, type MIM:230500
I

Gangliosidosis,
generalized GM1, type MIM:230600
II

Mucopolysaccharidosis IVB MIM:253010

Cross-references

Biochemical Pathways;
map number(s) B4

PROSITE PDOC00495 ; PDOC00531 ; PDOC00910

BRENDA 3.2.1.23

PUMA2 3.2.1.23

PRIAM enzyme-specific profiles 3.2.1.23

Kyoto University LIGAND chemical database 3.2.1.23

IUBMB Enzyme Nomenclature 3.2.1.23

KF GG ENZYME: 3.2.1.23

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Entry	EC 3.2.1.23	Enzyme
Name	beta-galactosidase; lactase; beta-lactosidase; maxilact; hydrolact; beta-D-lactosidase; S 2107; lactozym; trilactase; beta-D-galactanase; oryzatym; sumiklat	
Class	Hydrolases Glycosidases Glycosidases, i.e. enzymes hydrolysing O- and S-glycosyl compounds	
Sysname	beta-D-galactoside galactohydrolase	
Reaction	Hydrolysis of terminal non-reducing beta-D-galactose residues in beta-D-galactosides	
Other reac	R01105 R01678 R01679 R03355 R03616 R04633 R04783 R05112 R05994 R06010 R06098 R06099 R06111 R06144 R06202	
Comment	Some enzymes in this group hydrolyse alpha-L-arabinosides; some animal enzymes also hydrolyse beta-D-fucosides and beta-D-glucosides; cf. EC 3.2.1.108 lactase.	
Pathway	PATH: map00052 Galactose metabolism PATH: map00511 N-Glycan degradation PATH: map00531 Glycosaminoglycan degradation PATH: map00561 Glycerolipid metabolism PATH: map00600 Sphingolipid metabolism PATH: map00604 Glycosphingolipid biosynthesis - ganglioseries PATH: map01032 Glycan structures - degradation	
Ortholog	KO: K01190 beta-galactosidase	
Genes	HSA: 2720(GLB1) 3938(LCT) MMU: 12091(Glb1) 226413(Lct) RNO: 116569(Lct) 316033(Glb1_mapped) CFA: 403873(GLB1) DME: CG9092-PA(CG9092) CEL: T19B10.3 ATH: At1g72990(F3N23.19) At3g52840(F8J2.10) At5g20710(T1M15.110) CME: CMP078C DDI: DDB0188784 ECO: b0344(lacZ) b3076(ebgA) b3077(ebgC) ECJ: JW0335(lacZ) JW3048(ebgC) ECE: Z0440(lacZ) Z4429(ebgA) Z4430(ebgC) ECS: ECs0397 ECs3958 ECs3959	

3:2:1-23

KF[CG] ENZYME: 3.2.1.120

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Entry	EC 3.2.1.120	Enzyme
Name	oligoxyloglucan beta-glycosidase; isoprimeverose-producing oligoxyloglucan hydrolase; oligoxyloglucan hydrolase	
Class	Hydrolases Glycosidases Glycosidases, i.e. enzymes hydrolysing O- and S-glycosyl compounds	
Sysname	oligoxyloglucan xyloglucohydrolase	
Reaction	Hydrolysis of 1,4-beta-D-glucosidic links in oligoxyloglucans so as to remove successive isoprimeverose (i.e. alpha-xylo-1,6-beta-D-glucosyl-) residues from the non-reducing chain ends	
Reference 1	[PMID:4019436] Kato Y, Matsushita J, Kubodera T, Matsuda K. A novel enzyme producing isoprimeverose from oligoxyloglucans of <i>Aspergillus oryzae</i> . <i>J. Biochem. (Tokyo)</i> . 97 (1985) 801-10.	
Other DBs	IUBMB Enzyme Nomenclature: 3.2.1.120 ExPASy - ENZYME nomenclature database: 3.2.1.120 ERGO genome analysis and discovery system: 3.2.1.120 BRENDA, the Enzyme Database: 3.2.1.120 CAS: 97162-80-6	
LinkDB	All DBs	

=> Original format-----
DBGET integrated database retrieval system, GenomeNet

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NiceZyme View of ENZYME: EC 3.2.1.120

Official Name

Oligoxyloglucan beta-glycosidase.

Alternative Name(s)

Isoprimeverose-producing oligoxyloglucan hydrolase.

Reaction catalysed

Hydrolysis of 1,4-beta-D-glucosidic links in oligoxyloglucans so as to remove successive isoprimeverose (i.e. alpha-xylo-1,6-beta-D-glucosyl-) residues from the non-reducing chain ends

Cross-references

BRENDA	3.2.1.120
PUMA2	3.2.1.120
PRIAM enzyme-specific profiles	3.2.1.120
Kyoto University LIGAND chemical database	3.2.1.120
IUBMB Enzyme Nomenclature	3.2.1.120
IntEnz	3.2.1.120
MEDLINE	Find literature relating to 3.2.1.120
MetaCyc	3.2.1.120

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[All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.2.1.-](#)

[All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.2.--](#)

[All ENZYME / UniProtKB/Swiss-Prot entries corresponding to 3.-.--](#)

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